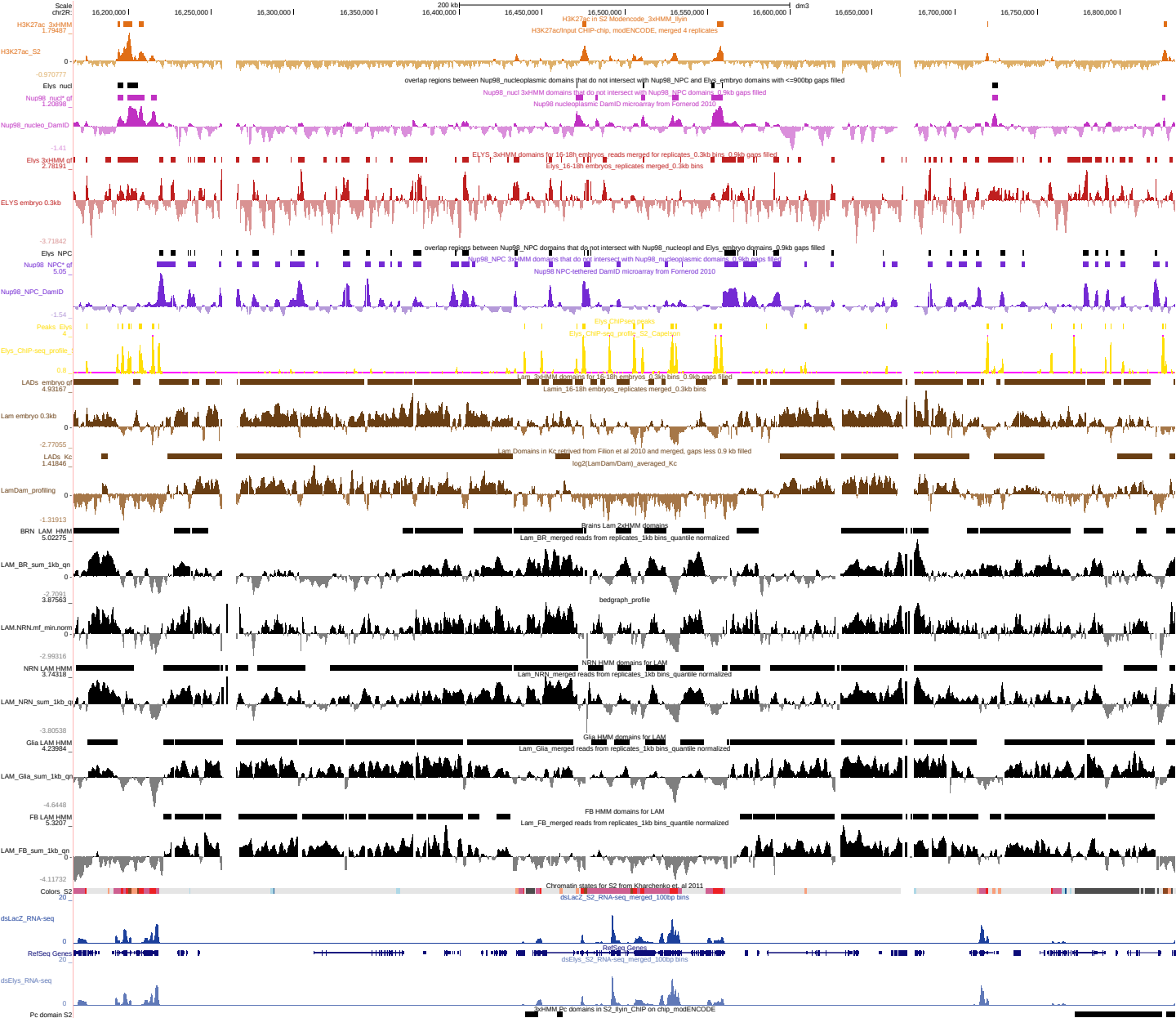
Scale
chr2R:
200 kb
dm3
16,200,000
16,250,000
16,300,000
16,350,000
16,400,000
16,450,000
16,500,000
16,550,000
16,600,000
16,650,000
16,700,000
16,750,000
16,800,000
H3K27ac_3xHMM
1.79487
H3K27ac in S2 Modencode_3xHMM_Ilyin
H3K27ac/Input ChIP-chip, modENCODE, merged 4 replicates
H3K27ac_S2
0
-0.970777
Elys_nucl
overlap regions between Nup98_nucleoplasmic domains that do not intersect with Nup98_NPC and Elys_embryo domains with <=900bp gaps filled
Nup98_nucl* of
1.20898
Nup98_nucl 3xHMM domains that do not intersect with Nup98_NPC domains_0.9kb gaps filled
Nup98 nucleoplasmic DamID microarray from Fornerod 2010
Nup98_nucleo_DamID
-1.41
Elys 3xHMM of
2.78191
ELYS_3xHMM domains for 16-18h embryos_reads merged for replicates_0.3kb bins_0.9kb gaps filled
Elys_16-18h embryos_replicates merged_0.3kb bins
ELYS embryo 0.3kb
-3.71842
Elys_NPC
overlap regions between Nup98_NPC domains that do not intersect with Nup98_nucleopl and Elys_embryo domains_0.9kb gaps filled
Nup98_NPC* of
5.05
Nup98_NPC 3xHMM domains that do not intersect with Nup98_nucleoplasmic domains_0.9kb gaps filled
Nup98 NPC-tethered DamID microarray from Fornerod 2010
Nup98_NPC_DamID
-1.54
Peaks_Elys
4
Elys_ChIPseq peaks
Elys_ChIP-seq_profile_S2_Capelson
Elys_ChIP-seq_profile_S
0.8
LADs_embryo of
4.93167
Lam_3xHMM domains for 16-18h embryos_0.3kb bins_0.9kb gaps filled
Lamin_16-18h embryos_replicates merged_0.3kb bins
Lam embryo 0.3kb
0
-2.77055
LADs_Kc
1.41846
Lam Domains in Kc retrived from Filion et al 2010 and merged, gaps less 0.9 kb filled
log2(LamDam/Dam)_averaged_Kc
LamDam_profiling
0
-1.31913
BRN_LAM_HMM
5.02275
Brains Lam 2xHMM domains
Lam_BR_merged reads from replicates_1kb bins_quantile normalized
LAM_BR_sum_1kb_qn
0
-2.7091
3.87563
bedgraph_profile
LAM.NRN.mf_min.norm
0
-2.99316
NRN LAM HMM
3.74318
NRN HMM domains for LAM
Lam_NRN_merged reads from replicates_1kb bins_quantile normalized
LAM_NRN_sum_1kb_qn
-3.80538
Glia LAM HMM
4.23984
Glia HMM domains for LAM
Lam_Glia_merged reads from replicates_1kb bins_quantile normalized
LAM_Glia_sum_1kb_qn
-4.6448
FB LAM HMM
5.3207
FB HMM domains for LAM
Lam_FB_merged reads from replicates_1kb bins_quantile normalized
LAM_FB_sum_1kb_qn
0
-4.11732
Colors_S2
20
Chromatin states for S2 from Kharchenko et al 2011
dsLacZ_S2_RNA-seq_merged_100bp bins
dsLacZ_RNA-seq
0
RefSeq Genes
20
RefSeq Genes
dsElys_S2_RNA-seq_merged_100bp bins
dsElys_RNA-seq
0
Pc domain S2
3xHMM Pc domains in S2_Ilyin_ChIP on chip_modENCODE